

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/582779

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) 3-6 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,779

DATE: 01/29/2001
TIME: 16:26:49

Input Set : A:\ES.txt
Output Set : N:\CRF3\01292001\I582779.raw

**Does Not Comply
Corrected Diskette Needed**

OK 3 <110> APPLICANT: Pompejus, Markus
4 Doval, Jose Luis Revuelta
5 Garcia, Maria Angeles Santos
7 <120> TITLE OF INVENTION: Orotidine-5'-phosphate decarboxylase gene, gene construct comprising
8 this gene and its use.
0 <130> FILE REFERENCE:
10 <140> CURRENT APPLICATION NUMBER: US 09/582,779
11 <141> CURRENT FILING DATE: 2000-07-03
13 <150> PRIOR APPLICATION NUMBER: Germany/19801120.2
14 <151> PRIOR FILING DATE: 1998-01-15
E--> 16 <160> NUMBER OF SEQ ID NOS: 5 6 (next page)
18 <170> SOFTWARE: WordPerfect version 6.1

ERRORED SEQUENCES

180 <210> SEQ ID NO: 3
181 <211> LENGTH: 18
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial sequence
185 <220> FEATURE:
186 <221> NAME/KEY: misc_feature
187 <222> LOCATION: 1 ... 18
W--> 189 <223> OTHER INFORMATION:
189 <400> SEQUENCE: 3
E--> 191 ytingnont ayathtgy
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 23
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial sequence
199 <220> FEATURE:
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: 1 ... 23
W--> 203 <223> OTHER INFORMATION:
203 <400> SEQUENCE: 4
E--> 205 taytgytnc qaryttrtc ncc
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 26
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial sequence
213 <220> FEATURE:
214 <221> NAME/KEY: misc_feature
215 <222> LOCATION: 1 ... 26
W--> 217 <223> OTHER INFORMATION:
217 <400> SEQUENCE: 5
E--> 219 ttyyinatht tygargaymg naartt
222 <210> SEQ ID NO: 6

Global error

see item 12 on Error Summary sheet
18 ← insert cumulative base total at right margin of each line

same error as above → *see item 10 on Error Summary sheet regarding n's*
total same error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/582,779

DATE: 01/29/2001
TIME: 16:26:50

Input Set : A:\ES.txt
Output Set: N:\CRF3\01292001\I582779.raw

223 <211> LENGTH: 19
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial sequence
227 <220> FEATURE:
228 <221> NAME/KEY: misc_feature
229 <222> LOCATION: 1 ... 19
W--> 231 <223> OTHER INFORMATION:
231 <400> SEQUENCE: 6
E--> 233 gcaatgataa raaatcctc

last sequence

total

*Suggestion: Consult new sequence
Rules for valid format*

VERIFICATION SUMMARY

DATE: 01/29/2001

PATENT APPLICATION: US/09/582,779

TIME: 16:26:51

Input Set : A:\ES.txt

Output Set: N:\CRF3\01292001\I582779.raw

L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:189 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:191 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:3
L:203 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:205 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:4
L:217 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:219 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:5
L:231 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:233 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:6
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (5) Counted (6)